

FIGURE 1

1 GAACCAGCCT GCACCGCGCTG GCTCCGGGTG ACAGCCGCGC GCCTCGGCCA
51 GGATCTGAGT GATGAGACGT GTCCCCACTG AGGTGCCCA CAGCAGCAGG
101 TGTGAGCAT GGGCTGAGAA GCTGGACCAG CACCAAAGGG CTGGCAGAAA
151 TGGGCGCCTG GCTGATTCT AGGCAGTTGG CGGCAGCAAG GAGGAGAGGC
201 CGCAGCTTCT GGAGCAGAGC CGAGACGAAG CAGTTCTGGA GTGCCTGAAC
251 GGCCCCCTGA GCCCTACCCG CCTGGCCCAC TATGGTCCAG AGGCTGTGGG
301 TGAGCCGCCT GCTGCGGCAC CGGAAAGCCC AGCTCTTGCT GGTCAACCTG
351 CTAACCTTTG GCCTGGAGGT GTGTTTGGCC GCAGGCATCA CCTATGTGCC
401 GCCTCTGCTG CTGGAAGTGG GGGTAGAGGA GAAGTTCATG ACCATGGTGC
451 TGGGCATTGG TCCAGTGCTG GGCTGGTCT GTGTCCCGCT CCTAGGCTCA
501 GCCAGTGACC ACTGGCGTGG ACGCTATGGC CGCCGCCGGC CCTTCATCTG
551 GGCAGTGCTCC TTGGGCATCC TGCTGAGCCT CTTTCTCATC CCAAGGGCCG
601 GCTGGCTAGC AGGGCTGCTG TGCCCGGATC CCAGGGCCCT GGAGCTGGCA
651 CTGCTCATCC TGGGCGTGGG GCTGCTGGAC TTCTGTGGCC AGGTGTGCTT
701 CACTCCACTG GAGGCCCTGC TCTCTGACCT CTTCCGGGAC CCGGACCAC
751 GTGCCAGGC CTACTCTGTC TATGCCTTCA TGATCAGTCT TGGGGGCTGC
801 CTGGGCTACC TCCTGCCTGC CATTGACTGG GACACCAGTG CCCTGGCCCC
851 CTACCTGGGC ACCCAGGAGG AGTGCCTTT TGGCCTGCTC ACCCTCATCT
901 TCCTCACCTG CGTAGCAGCC ACACTGCTGG TGGCTGAGGA GGCAGCGCTG
951 GGCCCCACCG AGCCAGCAGA AGGGCTGTGCG GCCCCCTCCT TGTCGCCCCA
1001 CTGCTGTCCA TGCCGGGCC GCTTGGCTTT CCGAACCTG GGCGCCCTGC
1051 TTCCCCGGCT GCACCAGCTG TGCTGCCGCA TGCCCGCAC CCTGCGCCGG
1101 CTCTTCGTGG CTGAGCTGTG CAGCTGGATG GCACTCATGA CCTTCACGCT
1151 GTTTTACACG GATTCGTGG GCGAGGGGCT GTACCAGGGC GTGCCAGAG
1201 CTGAGCCGGG CACCGAGGCC CGGAGACACT ATGATGAAGG CGTTCGGATG
1251 GGCAGCCTGG GGCTGTTCCCT GCAGTGCGCC ATCTCCCTGG TCTTCTCTCT
1301 GGTCATGGAC CGGCTGGTGC AGCGATTGG CACTCGAGCA GTCTATTGG
1351 CCAGTGTGGC AGCTTCCCT GTGGCTGCCG GTGCCACATG CCTGTCCCAC
1401 AGTGTGGCCG TGGTGACAGC TTCAGCCGCC CTCACCGGGT TCACCTTCTC

FIGURE 1 – continued

1451 AGCCCTGCAG ATCCTGCCCT ACACACTGGC CTCCCTCTAC CACCGGGAGA
1501 AGCAGGTGTT CCTGCCAAA TACCGAGGGG ACACTGGAGG TGCTAGCAGT
1551 GAGGACAGCC TGATGACCAG CTTCCTGCCA GGCCCTAACGC CTGGAGCTCC
1601 CTTCCCTAAT GGACACGTGG GTGCTGGAGG CAGTGGCCTG CTCCCACCTC
1651 CACCCGCGCT CTGCGGGGCC TCTGCCTGTG ATGTCTCCGT ACGTGTGGTG
1701 GTGGGTGAGC CCACCGAGGC CAGGGTGGTT CGGGGCCGGG GCATCTGCCT
1751 GGACCTCGCC ATCCTGGATA GTGCCTTCCT GCTGTCCCAG GTGGCCCCAT
1801 CCCTGTTTAT GGGCTCCATT GTCCAGCTCA GCCAGTCTGT CACTGCCTAT
1851 ATGGTGTCTG CCGCAGGCCT GGGTCTGGTC GCCATTTACT TTGCTACACA
1901 GGTAGTATTT GACAAGAGCG ACTTGGCCAA ATACTCAGCG TAGAAAACCTT
1951 CCAGCACATT GGGGTGGAGG GCCTGCCTCA CTGGGTCCCA GCTCCCCGCT
2001 CCTGTTAGCC CCATGGGGCT GCCGGGCTGG CCGCCAGTTT CTGTTGCTGC
2051 CAAAGTAATG TGGCTCTCTG CTGCCACCCCT GTGCTGCTGA GGTGCGTAGC
2101 TGCACAGCTG GGGGCTGGGG CGTCCCTCTC CTCTCTCCCC AGTCTCTAGG
2151 GCTGCCTGAC TGGAGGCCTT CCAAGGGGGT TTCAGTCTGG ACTTATACAG
2201 GGAGGCCAGA AGGGCTCCAT GCACTGGAAT GCGGGGACTC TGCAGGTGGA
2251 TTACCCAGGC TCAGGGTTAA CAGCTAGCCT CCTAGTTGAG ACACACCTAG
2301 AGAAGGGTTT TTGGGAGCTG AATAAACTCA GTCACCTGGT TTCCCATCTC
2351 TAAGCCCCTT AACCTGCAGC TTCGTTAAT GTAGCTCTTG CATGGAGTT
2401 TCTAGGATGA AACACTCCTC CATGGGATTG GAACATATGA AAGTTATTTG
2451 TAGGGGAAGA GTCCTGAGGG GCAACACACA AGAACAGGT CCCCTCAGCC
2501 CACAGCACTG TCTTTTGCT GATCCACCCC CCTCTTACCT TTTATCAGGA
2551 TGTGGCCTGT TGGTCCTTCT GTGCCATCA CAGAGACACA GGCATTTAAA
2601 TATTTAACTT ATTTATTTAA CAAAGTAGAA GGGAAATCCAT TGCTAGCTTT
2651 TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA
2701 GGTCCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT
2751 CTCCTGGGGT CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC
2801 TACTCATCCC AAATGATAAT TCCAAATGCT GTTACCCAAG GTTAGGGTGT

FIGURE 1 - continued

2851 TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT CTCAACGGCT TCCCTAACCA
2901 CCCCTCTTCT CTTGGCCCAG CCTGGTTCCC CCCACTTCCA CTCCCCCTCTA
2951 CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCCTACC
3001 CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT
3051 TGGAGCTACT GCAGGACCAAG AAGCACAAAG TGCGGTTCC CAAGCCTTG
3101 TCCATCTCAG CCCCCAGAGT ATATCTGTGC TTGGGGAATC TCACACAGAA
3151 ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG GAGGTCTTAT CTCTCAGGGG
3201 GGGGTTTAAG TGCCGTTGC AATAATGTAG TCTTATTAT TTAGCGGGGT
3251 GAATATTTA TACTGTAAGT GAGCAATCAG AGTATAATGT TTATGGTGAC
3301 AAAATTAAAG GCTTTCTTAT

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FIGURE 2

1 MVQRLWVSRL LRHRKAQLLL VNLLTFGLEV CLAAGITYVP PLLLEVGVVEE
51 KFMTMVLGIG PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL
101 FLIPRAGWLA GLLCPDPRPL ELALLILGVG LLDFCGQVCF TPLEALLSDL
151 FRDPDHCRQA YSVYAFMISL GGCLGYLLPA IDWDTSALAP YLGTQEECLF
201 GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH CCPCRARLAF
251 RNLGALLPRL HQLCCRMPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL
301 YQGVPRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG
351 TRAVYLASVA AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA
401 SLYHREKQVF LPKYRGDTGG ASSEDSLMTS FLPGPKGAP FPNGHVGAGG
451 SGLLPPPPPAL CGASACDVSV RVVVGEPTEA RVVPGRGICL DLAILDSAFL
501 LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ VVFDKSDLAK
551 YSA

FIGURE 3

DcSUT2 1 MENGTKELNKPQPPSSAAMQLQTPVQKIPTATWKLVLVAAIAAGVQFGWA 50
PROST03 1MVQRLWVSRLLRHKAQLLLNVNLTFGLEVCLA 33
51 LQLSLLTPYVQLLGIPHKWAAYIWLCGPISGMLVQPIVGYYSDHCQSSFG 100
34 AGITYVPPPLLLEVGVEEKFMTMVLGIGPVLGLCVPLLGSASDHWRGRYG 83
101 RRRPFIAASGAGCVAISVILIGFAADISYKAGDDMSKTLKPRAVTVFVIGF 150
84 RRRPFIAWLALGILLSLFLIPRAGWLAGLLCPDP....RPLELALLILGV 129
151 WILDVANNMLQGPCRALLADLCSDTTRMRSAANAFYSFFMAVGNILGYAA 200
130 GLLDFCGQVCFTPLEALLSDLFR.DPDHCRQAYSVYAFMISLGGCLGYLL 178
201 GSYN.NLYKLFPPFSKTHACDLYCANLKSCFIISIALLIIITVVALSVRE 249
179 PAIDWDTSALAPYLTQECLFGLLTILFLTCVAATLLVAEEAALGPTEP 228
250 NSGPPDDADAAEPPSSGKIPV..FGELLGALKDL....PRPMLLLLIVT 293
229 AEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAE 278
294 CLNWIAWFPFILFDTDWMGREIYGGT.....AGQGKLYDQGVVRAGALGL 337
279 LCSWMALMTFTLFYTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGL 328
338 LLNSVVLGLTSIAVEYLVRGVGGVKILWGFVNFILEAIGLVMTVVSKVAQ 387
329 FLQCAISLVFSLVMDRLVQRFGTRAV.....YLASVAAFPVAA 366
388 HQREHSANGQLLPPSAGVKAGALSLFSILGIPLSITYSIPFALASIYSSG 437
367 GATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKVFLPKYRG 416
438 SGAGQGLSLGVNLAIIVPQMIVSVLAGPFDSLFGGGNLPAFVVGAISAA 487
417 DTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPACGASAC 466
488 ISGVLAIVLLPKPSKDAASKLSSLGTYH..... 515
467 DVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLSQVAPSLFMGSTVQL 516

FIGURE 4

GAACCAGCCTGCACCGCCTGGCTCCGGGTGACAGCCGCCCTCGGCCAGGATCTGAGT
 1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
 CTTGGTCGGACGTGCGCACCGAGGCCACTGTCGGCGCGAGCCGGCTAGACTCA

 GATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGCTGAGAA
 61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
 CTACTCTGCACAGGGGTGACTCCACGGGTGTCGTCGTCACAACCTGTACCCGACTCTT

 GCTGGACCGGACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCTAGGCAGTTGG
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 CGACCTGGCGTGTTTCCCACCGTCTTACCCGCGGACCGACTAAGGATCCGTCAACC

 CGGCAGCAAGGAGGAGAGGCCGAGCTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGA
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 GCCGTCGTTCCCTCTCCGGCGTCGAAGACCTCGTCGCTCGGCTCTGCTTCGTCAAGACCT

 GTGCCTGAACGGCCCCCTGAGCCCTACCCGCTGGCCACTATGGTCCAGAGGCTGTGGG
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
 CACGGACTTGCCGGGGACTCGGGATGGCGGACCGGGTATAACCAGGTCTCCGACACCC

c M V Q R L W V -

TGAGCCGCTGCTGCGGACCGGAAAGCCAGCTTGTGCTGGTCAACCTGCTAACCTTTG
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
 ACTCGCGGACGACGCCGTGGCTTCGGGTGAGAACGACCGAGTTGGACGATTGGAAAC

c S R L L R H R K A Q L L L V N L L T F G -

GCCTGGAGGTGTGTTGGCCGCAGGCATCACCTATGTGCCGCTCTGCTGCTGGAAAGTGG
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
 CGGACCTCCACACAAACCGCGTCCGTAGTGGATACACGGCGGAGACGACGACCTTCACC

c L E V C L A A G I T Y V P P L L L E V G -

GGGTAGAGGAGAAGTTCATGACCATGGTGTGGCATTGGTCCAGTGCTGGGCTGGTCT
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
 CCCATCTCCTCTCAAGTACTGGTACCAACGACCCGTAACCGAGTCACGACCCGGACAGA

c V E E K F M T M V L G I G P V L G L V C -

GTGTCCCCTCTAGGCTCAGCCAGTGACCAACTGGCGTGGACGCTATGGCCGCCGCCGGC
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 CACAGGGCGAGGATCCGAGTCGGTCACTGGTACCGCACCTGCGATAACGGCGGGCGCG

c V P L L G S A S D H W R G R Y G R R R P -

CCTTCATCTGGCACTGTCCTGGCATCCTGCTGAGCCTTTCTCATCCAAAGGGCCG
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 GGAACTAGACCCGTGACAGGAACCGTAGGACGACTCGGAGAAAGAGTAGGGTCCCGGC

c F I W A L S L G I L L S L F L I P R A G -

GCTGGCTAGAGGGCTGCTGTGCCCCGATCCAGGCCCTGGAGCTGGCACTGCTCATCC
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 CGACCGATCGTCCCGACACGGGCCTAGGGTCCGGGACCTGCGACCGTGACGAGTAGG

c W L A G L L C P D P R P L E L A L L I L -

TGGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC
 661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
 ACCCGCACCCGACGACCTGAAGACACCGGTCCACACGAAGTGAGGTGACCTCCGGGACG

c G V G L L D F C G Q V C F T P L E A L L -

FIGURE 4 – continued

TCTCTGACCTCTCCGGGACCCGGACCCTGTCGCCAGGCCTACTCTGTCTATGCCTTCA
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
 AGAGACTGGAGAAGGCCCTGGCCTGGTGACAGCGGTCGGATGAGACAGATAACGGAAGT

 c S D L F R D P D H C R Q A Y S V Y A F M -

 TGATCAGTCTTGGGGCTGCCTGGCTACCTCTGCCATTGACTGGACACCAGTG
 781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
 ACTAGTCAGAACCCCCGACGGACCCGATGGAGGACGGACGGTAAC TGACCCTGTGGTCAC

 c I S L G G C L G Y L L P A I D W D T S A -

 CCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTGCCCTGCTCACCCCTCATCT
 841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 GGGACCGGGGGATGGACCCGTGGTGCCTCCTCACGGAGAAACCGGACGAGTGGAGTAGA

 c L A P Y L G T Q E E C L F G L L T L I F -

 TCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCG
 901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
 AGGAGTGGACGACATCGTCGGTGTGACGACCAACCGACTCCTCCGTCGACCCGGGTGGC

 c L T C V A A T L L V A E E A A L G P T E -

 AGCCAGCAGAAGGGCTGTGCGGCCCCCTCCCTGTCGCCCCACTGCTGTCCATGCCGGGCC
 961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
 TCGGTCGTCTCCGACAGCCGGGGAGGAACAGCGGGGTGACGACAGGTACGGCCCGGG

 c P A E G L S A P S L S P H C C C P C R A R -

 GCTTGGCTTCCGAACCTGGCGCCCTGCTTCCCCGGCTGCACCAAGCTGTGCTGCCGCA
 1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
 CGAACCGAAAGGCCTGGACCCCGGGACGAAGGGCCGACGTGGTCGACACGACGGCGT

 c L A F R N L G A L L P R L H Q L C C R M -

 TGCCCCGCACCCCTGCGCCGGCTTCTGTTGGCTGAGCTGTGAGCTGGATGGCACTCATGA
 1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
 ACGGGGCGTGGGACGCGGCCGAGAACGACCCGACTCGACACGTCGACCTACCGTGAGTACT

 c P R T L R R L F V A E L C S W M A L M T -

 CCTTCACGCTGTTTACACGGATTCGTGGCGAGGGCTGTACCGGGCGTGCAGAG
 1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
 GGAAAGTGCACAAATGTGCCTAAAGCACCCGCTCCCGACATGGTCCCACGGGTCTC

 c F T L F Y T D F V G E G L Y Q G V P R A -

 CTGAGCCGGGACCGAGGCCGGAGACACTATGATGAAGGCCTCGGATGGCAGCCTGG
 1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
 GACTCGGCCGTGGCTCCGGCCTCTGTGATACTACTTCCGCAAGCCTACCGTCGGACC

 c E P G T E A R R H Y D E G V R M G S L G -

 GGCTGTTCTGCACTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGC
 1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
 CCGACAAGGACGTCACGCGGTAGAGGGACCAAGAGAGACCAAGTACCTGGCCGACCAACG

 c L F L Q C A I S L V F S L V M D R L V Q -

 AGCGATTGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGCTGCCG
 1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380
 TCGCTAAGCCGTGAGCTCGTCAGATAAACCGGTACACCGTCGAAAGGGACACCGACGGC

 c R F G T R A V Y L A S V A A F P V A A G -

FIGURE 4 - continued

1381 GTGCCACATGCCTGCCCCAACAGTGTGGCCGTGGTACAGCTTCAGCCGCCCTACCGGGT
 1440 CACGGTGTACGGACAGGGTGTACACCGGACCAACTGTCGAAGTCGGCGGGAGTGGCCA
 c A T C L S H S V A V V T A S A A L T G F -
 1441 TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCCTCCCTTACACCACGGGAGA
 1500 AGTGGAAAGAGTCGGACGTCTAGGACGGATGTGACCGGAGGGAGATGGTGGCCCTCT
 c T F S A L Q I L P Y T L A S L Y H R E K -
 1501 AGCAGGTGTTCCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC
 1560 TCGTCCACAAGGACGGTTATGGCTCCCCGTGACCTCCACGATCGTCACTCCTGTCGG
 c Q V F L P K Y R G D T G G A S S E D S L -
 1561 TGATGACCAGCTTCTGCCAGGCCCTAACGCCCTGGAGCTCCCTCCCTAACGGACACGTGG
 1620 ACTACTGGTCGAAGGACGGTCCGGATTGGACCTCGAGGGAGGGATTACCTGTGCACC
 c M T S F L P G P K P G A P F P N G H V G -
 1621 GTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGGGGGCTCTGCCTGTG
 1680 CACGACCTCCGTACCGGACGAGGGTGGAGGTGGGGCCGAGACGCCCGAGACGGACAC
 c A G G S G L L P P P P A L C G A S A C D -
 1681 ATGTCTCCGTACGTGTGGTGGGTGAGGCCACCGAGGGCAGGGTGGTTCCGGCCGG
 1740 TACAGAGGCATGCACACCACCCACTCGGGTGGCTCCGGTCCACCAAGGGCCGGCC
 c V S V R V V V G E P T E A R V V P G R G -
 1741 GCATCTGCCCTGGACCTCGCCATCCTGGATAGTGCCTTCTGCTGTCCCAGGTGGCCCAT
 1800 CGTAGACGGACCTGGAGCGGTAGGACCTATCACGGAAAGGACGACAGGTCCACGGGTA
 c I C L D L A I L D S A F L L S Q V A P S -
 1801 CCCTGTTATGGGCTCCATTGTCAGCTCAGCCAGTGTCACTGCCTATATGGTGTCTG
 1860 GGGACAAATACCGAGGTAACAGGTCGAGTCGGTCAGACAGTGACGGATATAACCACAGAC
 c L F M G S I V Q L S Q S V T A Y M V S A -
 1861 CCGCAGGGCTGGGTCTGGTCGCCATTACTTACAGGTACACAGGTAGTATTTGACAAGAGCG
 1920 GGCGTCCGGACCCAGACCAGCGGTAAATGAAACGATGTGTCCATATAACTGTTCTCGC
 c A G L G L V A I Y F A T Q V V F D K S D -
 1921 ACTTGGCCAAATACTCAGCGTAGAAAATTCAGCACATTGGGTGGAGGGCCTGCCTCA
 1980 TGAACCGGTTATGAGTCGCATCTTGAGGTGTAACCCCACCTCCGGACGGAGT
 c L A K Y S A *
 1981 CTGGGCCCCAGCTCCCCGCTCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGTT
 2040 GACCCAGGGTCGAGGGCGAGGACAATCGGGTACCCGACGGCCGACGGCGGTCAA

FIGURE 4 - continued

2041 CTGTTGCTGCCAAAGTAATGTGGCTCTGCTGCCACCCCTGTGCTGAGGTGCGTAGC 2100
 GACAACGACGGTTCAATTACACCGAGAGACGACGGTGGGACACGACACTCCACGCATCG
 TGCACAGCTGGGGCTGGGGCGTCCCTCTCTCTCCCCAGTCAGGGCTGCCTGAC 2160
 ACGTGTCGACCCCCGACCCCGCAGGGAGAGGAGAGAGGGTCAGAGATCCGACGGACTG
 TGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATAACAGGGAGGCCAGAAGGGCTCCAT 2220
 ACCTCCCGAACGGTCCCCCAAAGTCAGACCTGAATATGTCCCTCCGGCTTCCCGAGGTA
 GCACCTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT 2280
 CGTGACCTTACGCCCTGAGACGTCCACCTAATGGTCCGAGTCCAATTGTCGATCGGA
 CCTAGTTGAGACACACCTAGAGAAGGGTTTGGGAGCTGAATAAAACTCAGTCACCTGGT 2340
 GGATCAACTCTGTGTGGATCTTCCAAAACCTCGACTTATTGAGTCAGTGGACCA
 TTCCCACATCTCTAACGCCCTTAACCTGCAGCTCGTTAATGTAGCTTGCATGGGAGTT 2400
 AAGGGTAGAGATTGGGAATTGGACGTCAAGCAAATTACATCGAGAACGTACCCCTCAA
 TCTAGGATGAAACACTCCTCCATGGGATTGAAACATATGAAAGTTATTTGTAGGGGAAGA 2460
 AGATCCTACTTTGTGAGGAGGTACCCCTAAACTTGTATACTTTCAATAAACATCCCTCT
 GTCCTGAGGGCAACACACAAGAACAGGTCCCTCAGCCACAGCACTGTCTTTGCT 2520
 CAGGACTCCCGTTGTGTGTTCTGGTCCAGGGAGTCGGTGTGACAGAAAAACGA
 GATCCACCCCCCTTTACCTTATCAGGATGTGGCTGTTGGTCCTCTGTTGCCATCA 2580
 CTAGGTGGGGGAGAATGGAAAATAGTCCTACACCGGACAACCAGGAAGACAACGGTAGT
 CAGAGACACAGGCATTTAAATATTTAACTTATTAAACAAAGTAGAAGGGAATCCAT 2640
 GTCTCTGTGTCCGTAAATTATAAAATTGAATAAAATAATTGTTCATCTCCCTTAGGTA
 TGCTAGCTTTCTGTGTTGGTGTCTAATATTGGTAGGGTGGGGATCCCCAACATCA 2700
 ACGATCGAAAAGACACAACCACAGATTATAAACCCATCCCACCCCTAGGGTTGTTAGT
 GGTCCCCCTGAGATAGCTGGTCACTGGCTGATCATTGCCAGAATCTCTCTGGGGT 2760
 CCAGGGACTCTACGACCAGTAACCGACTAGTAACGGTCTTAGAAGAAGAGGACCCCA
 CTGGCCCCCAAATGCCAACCCAGGACCTGGAAATTCTACTCATCCAAATGATAAT 2820
 GACCGGGGGGTTTACGGATTGGTCCCTGGAACCTTAAGATGAGTAGGGTTACTATTA
 TCCAAATGCTGTTACCAAGGTTAGGGTGTGAAGGAAGGTAGAGGGTGGGCTTCAGGT 2880
 AGGTTACGACAATGGGTTCAATCCCACAACTCCTCCATCTCCACCCGAAGTCCA
 CTCAACGGCTCCCTAACCAACCCCTCTCTCTGGCCAGCCTGGTTCCCCCACTTCCA 2940
 GAGTTGCCGAAGGGATTGGTGGGGAGAAGAGAACCGGGTGGACCAAGGGGGTGAAGGT
 CTCCCCCTACTCTCTAGGACTGGCTGATGAAGGCAGTGCCTAAATTCCCCTTAC 3000
 GAGGGAGATGAGAGAGATCCTGACCCGACTACTTCGACGGTTAAAGGGGATGG

FIGURE 4 - continued

3001 CCCAACTTCCCCAACCCCCAACCTCCACAGCTCCACAACCCCTGTTGGAGCTACT
GGGTTGAAAGGGATGGGGTTGAAAGGGTGGTCGAGGTGTTGGACAAACCTCGATGA 3060

3061 GCAGGACCAGAACAAAGTGCAGTTCCAAGCCTTGTCATCTCAGCCCCAGAGT
CGTCCTGGCTTCGTGTTCACGCCAACAGGTTCGAACAGGTAGAGTCGGGGTCTCA 3120

3121 ATATCTGTGCTTGGGAATCTCACACAGAAA CTCAGGAGCACCCCTGCCTGAGCTAAGG
TATAGACACGAACCCCTTAGAGTGTGTTGAGTCCTCGTGGGGACGGACTCGATTCC 3180

3181 GAGGTCTTATCTCAGGGGGGTTAACGTGCCGTTGCAATAATGTCGTCTTATTAT
CTCCAGAACAGAGTCCCCCCCCAACATTACGGCAAACGTTATTACAGCAGAATAATA 3240

3241 TTAGGGGTGAATATTTTACTGTAAGTGAGCAATCAGAGTATAATGTTATGGTGAC
AATCGCCCCACTTATAAAATATGACATTCACTCGTTAGTCTCATATTACAAATACACTG 3300

3301 AAAATTAAAGGCTTCTTAT
TTTTAATTCCGAAAGAATA 3320

SCANNED, # 12

Figure 5
Expression of Prost 3 in Human Tissue

